Claims:

1. An isolated nucleotide sequence, characterized in that said sequence encodes a ROB5 protein, or a fragment thereof.

2. An isolated nucleotide sequence characterized in that said isolated nucleotide sequence is selected from:

a) a *ROB5* gene as shown in SEQ ID NO: 1, or a complement thereof;

b) a nucleotide sequence encoding a peptide with at least 50% identity to a peptide encoded by the nucleotide sequence of a), or a complement thereof;

wherein said nucleotide sequence or complement thereof encodes a protein or a part thereof, that alters a stress response and / or growth potential of a transgenic plant exogenously expressing said nucleotide sequence compared to an unmodified plant.

3. The isolated nucleotide sequence according to claim 2 characterized in that said nucleotide sequence or a complement thereof encodes a protein having at least 70 % sequence identity to the *ROB5* gene shown in SEQ ID NO: 1 or a complement thereof.

4. The isolated nucleotide sequence according to claim 2 characterized in that said nucleotide sequence or a complement thereof encodes a protein having at least 90 % sequence identity to the *ROB5* gene shown in SEQ ID NO: 1 or a complement thereof.

5. The isolated nucleotide sequence according to claim 2 characterized in that said nucleotide sequence or a complement thereof encodes a protein having at least 95 % sequence identity to the *ROB5* gene shown in SEQ ID NO: 1 or a complement thereof.

6. An isolated nucleotide sequence, characterized in that said isolated

nucleotide sequence is selected from the group consisting of:

a) a *ROB5* gene according to SEQ ID NO: 1, or a complement thereof;

b) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of a), or a complement thereof;

wherein said nucleotide sequence or complement thereof encodes a protein or part thereof that alters a stress response and / or growth potential of a transgenic plant exogenously expressing said nucleotide sequence compared to an unmodified plant.

7. The isolated nucleotide sequence of claim 2, characterized in that expression of said nucleotide sequence confers on said transgenic plant an altered stress response selected from the group consisting of: increased tolerance to heat, increased tolerance to cold; increased tolerance to frost, increased tolerance to drought, increased tolerance to flood, increase resistance to pests, increased resistance to disease.

8. The isolated nucleotide sequence of claim 2, characterized in that expression of said nucleotide sequence confers on said transgenic plant an altered growth potential selected from the group consisting of: faster growth rate, slower growth rate, larger biomass, and smaller biomass.

9. The isolated nucleotide sequence according to claim 2 characterized in that the nucleotide sequence is derived from a bromegrass plant.

10. The isolated nucleotide sequence according to claim 2 characterized in that expression of said nucleotide sequence in a plant causes said plant to exhibit higher survival rate in adverse conditions compared to an unmodified plant.

11. An isolated and purified peptide characterized in that said isolated and purified peptide is encoded by the nucleotide sequence according to claim 2, or

a complement thereof.

12. A DNA expression cassette characterized in that said DNA expression cassette comprises the nucleotide sequence according to claim 2, operably linked to a promoter.

13. A construct characterized in that the construct comprises a vector and the nucleotide sequence according to claim 2, or the DNA expression cassette according to claim 12.

14. The construct according to claim 13 characterized in that said nucleotide sequence is operably linked to a promoter.

15. The construct according to claim 14 characterized in that said promoter is selected from the group consisting of: a constitutive promoter, an inducible promoter, an organ specific promoter, a strong promoter, a weak promoter, and a stress induced promoter.

16. A plant cell characterized in that said plant cell is transformed with the construct according to claim 13.

17. A transgenic plant characterized in that said transgenic plant is derived from regeneration of said plant cell according to claim 16.

18. The transgenic plant according to claim 17 characterized in that said transgenic plant is selected from a species of grain producing crop, a fruit or vegetable species, and a horticultural species.

19. The transgenic plant according to claim 18 characterized in that said transgenic plant is a species selected from the group consisting of: canola, flax, and potato.

20. A method of genetically modifying a plant, characterized in that the method comprises the steps of:

(a) introducing into a plant cell capable of being transformed and regenerated into a whole plant a construct comprising, in addition to the DNA sequences required for transformation and selection in plants, a nucleotide sequence according to claim 2, operably linked to a promoter; and

(b) recovery of a plant which contains said nucleotide sequence.

21. The method according to claim 20 characterized in that said plant exhibits an altered stress tolerance and / or altered growth potential compared to an unmodified plant.

22. The method according to claim 21 characterized in that said plant exhibits an altered stress response selected from the group consisting of: increased tolerance to heat, increased tolerance to cold; increased tolerance to frost, increased tolerance to drought, increased tolerance to flood, increase resistance to pests, increased resistance to disease.

23. The method according to claim 20 characterized in that said plant exhibits one or more growth characterisitics that are altered compared to an unmodified plant, the growth characteristics selected from the group consisting of: faster growth rate, slower growth rate, larger biomass, and smaller biomass,

24. The method according to claim 20 characterized in that said nucleotide sequence is oriented in a sense direction relative to a promoter.

25. The method according to claim 20 characterized in that said nucleotide sequence is oriented in an antisense direction relative to a promoter.

26. A method of identifying and isolating a DNA sequence substantially

homologous to the nucleotide sequence of claim 2, characterized in that said method comprises the steps of:

synthesizing a degenerate oligonucleotide primer than can hybridize to the nucleotide sequence of claim 1 or 2 under stringent conditions;

labelling said degenerate oligonucleotide primer;

using said labelled degenerate oligonucleotide primer as a probe to screen a DNA library for said substantially homologous DNA sequence; and

isolating the substantially homologous DNA sequence from the library.

27. An isolated nucleotide sequence characterized in that said isolated nucleotide sequence is obtainable by the method according to claim 26.

28. A pair of primers characterized in that said primers hybridize to selected portions of the nucleotide sequence of claim 2, for amplifying a region of DNA between said primers by polymerase chain reaction.

29. Use of an isolated nucleotide sequence according to claim 2, characterized in that said use is for generating a transgenic plant that exhibits an altered stress response compared to an unmodified plant.

30. Use of an isolated nucleotide sequence according to claim 2, characterized in that said use is for generating a transgenic plant that exhibits an altered growth potential compared to an unmodified plant.

31. A method of producing a transgenic plant with a modified stress response and / or growth potential, characterized in that the method comprises the steps of:

(a) introducing into a plant cell capable of being transformed and regenerated into a whole plant a construct comprising, in addition to the DNA sequences required for transformation and selection in plants, a nucleotide sequence derived from a *ROB5* gene operably linked to a promoter; and

(b) recovery of a plant which contains said nucleotide sequence and has a modified stress response and / or growth potential compared to an unmodified plant.

32. A method according to claim 31, characterized in that said nucleotide sequence encodes a peptide having at least 50% identity to the peptide indicated in SEQ ID NO: 1, or a part thereof, or a complement thereof.

33. A method according to claim 31, characterized in that said nucleotide sequence encodes a peptide having at least 70% identity to the peptide indicated in SEQ ID NO: 1, or a part thereof, or a complement thereof.

34. A method according to claim 31, characterized in that said nucleotide sequence encodes a peptide having at least 90% identity to the peptide indicated in SEQ ID NO: 1, or a part thereof, or a complement thereof.

35. A method according to claim 31, characterized in that said nucleotide sequence encodes a peptide having at least 95% identity to the peptide indicated in SEQ ID NO: 1, or a part thereof, or a complement thereof.

36. A method according to claim 31, characterized in that said nucleotide sequence encodes a peptide having at least 99% identity to the peptide indicated in SEQ ID NO: 1, or a part thereof, or a complement thereof.

37. A method according to claim 31, characterized in that said nucleotide sequence is the nucleotide sequence indicated in SEQ ID NO: 1, or a part thereof, or a complement thereof, or a nucleotide sequence that binds under stringent conditions to the nucleotide sequence indicated in SEQ ID NO: 1, or a part thereof, or a complement thereof

38. A method according to claim 31, characterized in that said nucleotide

sequence is expressed in a sense direction for complementary inhibition of an endogenous *ROB5* gene in said plant, said plant having a decreased stress tolerance and / or a decreased growth potential compared to an unmodified plant.

39. A method according to claim 38, characterized in that said nucleotide sequence is a mutated *ROB5* gene.

40. A method according to claim 31, characterized in that said nucleotide sequence is expressed in an antisense direction for antisense inhibition of an endogenous *ROB5* gene of said plant, said plant having a decreased stress tolerance and / or a decreased growth potential compared to an unmodified plant.

41. A method according to claim 31, characterized in that said nucleotide sequence is overexpressed in a sense direction, said plant having an increased stress tolerance and / or an increased growth potential compared to an unmodified plant.

42. A method according to claim 31, characterized in that said promoter comprises a transcriptional regulatory region normally in operable association with an endogenous *ROB5* gene or homologue thereof.

43. A method according to claim 31, characterized in that said promoter comprises a transcriptional regulatory region that is not normally in operable association with an endogenous *ROB5* gene or homologue thereof.

44. A method according to claim 31, characterized in that said promoter is selected from the group consisting of: a constitutive promoter, an inducible promoter, an organ specific promoter, a strong promoter, a weak promoter, and an endogenous *ROB5* promoter.

45. A method of identifying a plant that has been successfully transformed with a construct, characterized in that the method comprises the steps of:

(a) introducing into plant cells capable of being transformed and regenerated into whole plants a construct comprising, in addition to the DNA sequences required for transformation and selection in plants, a nucleotide sequence derived from a *ROB5* gene and encoding at least part of a *ROB5* gene product, operably linked to a promoter;

(b) regenerating said plant cells into whole plants; and

(c) inspecting the plants to determine those plants successfully transformed with said construct, and expressing said nucleotide sequence.

46. A method according to 45, characterized in that said construct is bicistronic and further comprises a second DNA expression cassette for generating a transcript unrelated to said nucleotide sequence derived from a *ROB5* gene.

47. A transgenic plant characterized in that said transgenic plant is generated by the method according to any one of claims 31 to 46.

48. A bicistronic vector characterized in that said bicistronic vector comprises a first nucleotide sequence according to claim 2 operatively linked to a first tissue-specific promoter, and a second nucleotide sequence according to claim 2 operatively linked to a second tissue-specific promoter.

49. The bicistronic vector according to claim 48, characterized in that expression of said vector in a transgenic plant induces alternative stress tolerance and growth potential characteristics in different tissues of said plant according to said first and second nucleotide sequences and said operatively linked first and second promoters.

50. The bicistronic vector according to claim 49, characterized in that said first nucleotide sequence is oriented in a sense direction relative to said first promoter, and said second nucleotide sequence is oriented in an antisense direction relative to said second promoter.

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51. The bicistronic vector according to claim 49, characterized in that said first nucleotide sequence encodes a biologically active form of a ROB5 protein or a part thereof, and said second nucleotide sequence encodes a biologically inactive form of a ROB5 protein or a part thereof.

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52. A transgenic part characterized in that said transgenic plant is transformed with a bicistronic vector according to any one of claims 48 to 51.